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TECH CENTER



1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/502,426B

DATE: 05/28/2003

TIME: 15:14:18

Input Set : A:\11696-070001.txt

Output Set: N:\CRF4\05282003\I502426B.raw

3 <110> APPLICANT: Azpiroz, Ricardo  
 4 Choe, Sunghwa  
 5 Feldmann, Kenneth A.  
 7 <120> TITLE OF INVENTION: DWF4 POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF  
 9 <130> FILE REFERENCE: 11696-070001  
 11 <140> CURRENT APPLICATION NUMBER: US 09/502,426B  
 12 <141> CURRENT FILING DATE: 2000-02-11  
 14 <150> PRIOR APPLICATION NUMBER: US 60/119,657  
 15 <151> PRIOR FILING DATE: 1999-02-11  
 17 <150> PRIOR APPLICATION NUMBER: US 60/119,658  
 18 <151> PRIOR FILING DATE: 1999-02-11  
 20 <160> NUMBER OF SEQ ID NOS: 30  
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 6888  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Arabidopsis thaliana  
 29 <400> SEQUENCE: 1

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 31 tattctgttc acatgatttg agtttggttc tcaatttgga ttccaagata attaaatatt 120  
 32 aaaattcatt taaaatattt acaagtaatt aattatcttt acattgtatt gttataacaa 180  
 33 aatatctatc tttggtatat gagaaaatat ggagtttgga atttataata ataaaggaaa 240  
 34 taatcgattc catttggttg gattacacag ttaagttttt gtgtttcttt tgttatatgt 300  
 35 atatgagtaa atcaaaaaga gtattgattg aagtgtaaac atatttcgtt atgaccccca 360  
 36 aaaaaaaaaa aaaaacaaac aaacaaaccc cccccccgat atagtttttg gttctggatt 420  
 37 aggttttatt gatcataatt acatgcatca tttctttgat tactatgaag attttcttac 480  
 38 caattaaaaat ttcgaattca tatctcttga ttatttaaatt aaatacgagt gtgaatatcc 540  
 39 gtttatcgat cactccaatc atgattatga ttcttgtgct aatccagcaa attattaaca 600  
 40 agagtattga gaaaaaacg aaaataagaa aagggaagaa gtagtgacc atggagtag 660  
 41 tgaataatta tcaaaagaaa taagagatga caacaaaag gttgtggaat aatggtcct 720  
 42 gccagctttc tctcacaatc aatatcgacc ctatttggat tttctggata ttcgttaaaa 780  
 43 tttgcgataa cgattgtgaa aaatatatta tttgttagct gatctcaata ttatgttcca 840  
 44 ggtatttgca taatcttctg tttaaagcat attttgtctt tctttttgtt tcgtttctct 900  
 45 taactatata ttatcgcgga tatatgataa caatgatata tcacaaaaca attgtctggg 960  
 46 accattttga ataaactttt tctcaaacat tacgggacac tggactcgac ccttaaaata 1020  
 47 cgattttaca gcgtcactag ttgagattac tagcataaag cataaaggac ccgttcaagc 1080  
 48 tatttatata aagttacaaa ctgaatatag cttgaaatcc tttagaaaat tttggaatta 1140  
 49 ccggttggtta tgtaaataa gatttagtgg taaacaaata tgtaaatcaa ttagtggtca 1200  
 50 acatatacat aattccttac agaaaaaaca aacttaagag aagttaacat atccatatat 1260  
 51 gggatgctta tacctttcac gtatgctata ctagagacta aagaatagtt atgtgatgtc 1320  
 52 gataaatgaa attcacacgc gtggtaataa ttatgggacc gtatgttacg atcactgcaa 1380  
 53 atatcattct tggttggtca acaataaaaa caaaaacaag aaaaaagaa aacgattttt 1440  
 54 cttggattcc attcaatgat ctaaaatgca tagatctttt gggttacagt ttcgaagtcc 1500

P.6

ENTERED

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55 tctacaagcg tgtaaccatc tgcaactatt aaattgcttt ctttaatgca tctttaacat 1560
56 atttattggt agttggaatt taataagagc gaacttgtaa cattacaata tttatattag 1620
57 atactagtat gtgattattc caaatacata ctttgatgt ttaaacttaa tcttgtttct 1680
58 tcctacggta taaatattaa tcatcgaggt aaaaaaagtt ttgtcttatt ttgcgcgatgc 1740
59 atgaaggata aacctaatga ctttaatttt ttgaaaatgt aaccttttta ctcatagatt 1800
60 aattaccgta tgtttttggt gccataatga cagcctctac aactgtgata gtcaattttt 1860
61 tctgcaaata ttaaattagg aattcaatgc tactatcaat agaagaaaca gctgagtatt 1920
62 acattttaat ttaaagacaa aatttttgaa aaatgttata atttctaaca atattattaa 1980
63 aatatgatgc ctataatgta tttcctatgt tcttaaaata ttttttttta tatttagtta 2040
64 taaatacatt atgaaccaat aatagttggt gaattcaaat atctccatta atattttttg 2100
65 aaatctacaa attattaata tttagtcaat aacaatgcat agaaagtctc aaaaaaaatt 2160
66 ttgttaacag aaacttccaa attttttttt tttatggaac aagaaataac agatagaaaa 2220
67 ctattttggt gtggaatgga agtagtaata tacattaagc aaatttttaa aaattatata 2280
68 agcctatacg cgtcaaaagt atgttatcta gtaggtgtaa ttaataatgc atgggtgcgat 2340
69 tcagaattgg gacaacaatg aaaacggaat taaaatatta actttaaaat aaataaaaaat 2400
70 ttgagtaaatt gtgttttctg actattgagg ggcaaaaaaa agacaatgcc aaaagtctac 2460
71 gggtttgact gtccagttcg gtaataatct aataactctg tctttgaccg cacgctcgtg 2520
72 taggggtcct tctgacattt tcaactgttct acccctactc gtgagcccac cttttccca 2580
73 tatcctaagg gtaatttttg aaatcccaat ttaaaccgat tgagaccgta ccggacttcc 2640
74 tgggattctc ctggagcatt tatcaaaaaa tattagcacg aatgggttta ttaattttaa 2700
75 aactcacacg ttgatcagat aaaatttcat aaacactttt acgatggatt cgtacgatct 2760
76 atctaattgac tttttttttt ctaccacggt ggatgaaagt tatagtacta ttagccagag 2820
77 acaattgatt atagatatat ccattaatcc atgatattta tgatataaat agtgtttaa 2880
78 ctattttcagc atcgcagctt tctgcaactt ttgtttttta ttaagagtt taataaataa 2940
79 aagtattaaa aggagcataa cgaggcaaca aaagtaatga acacggagaa acaaaaagcca 3000
80 tgaagctcat tggtagttt aagcttaata agaagatttt attaaatttt aatgacgatg 3060
81 ataaqaatta tattttctga cttcttttaa acccctctt acaaacagaa gctccctttt 3120
82 tcagtagaag tccgattccc aatcttaaag acaaagccat tagaaagaga aagtgaagtga 3180
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89 ccaacgatcg tatcagctga tgctggactt aatagattca tattacaaaa cgaaggaagg 3600
90 ctctttgaat gtagttatcc tagaagtata ggtgggattc ttgggaaatg gtcgatgctt 3660
91 gttcttggtg gtgacatgca tagagatatg agaagtatct cgcttaactt cttaaagtac 3720
92 gcacgtctta gaactattct acttaaagat gttgagagac atactttggt tgttcttgat 3780
93 tcttggaac aaaactctat tttctctgct caagacgagg ccaaaaaggt ttttattttt 3840
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95 ttaattgaa cagtttacgt ttaatctaatt ggcaagcat ataattgagta tggatcctgg 3960
96 agaagaagaa acagagcaat taaagaaaga gtatgtaact ttcatgaaag gagttgtctc 4020
97 tgctcctcta aatctaccag gaactgctta tcataaagct cttcaggtac atttattttt 4080
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101 gaggatgaag cagagatgag taagagtgat catgttagga aacaaagaac agacgatgat 4320
102 cttttgggat gggtttgaa acattcgaat ttatcgacgg agcaaatctc cgatctcatt 4380
103 cttagtttgt tatttgccgg acatgagact tcttctgtag ccattgctct cgctatcttc 4440

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104 ttcttgcaag cttgccctaa agccgttgaa gagcttaggg taagataatt ataacagcac 4500
105 aagttaatta ctaccaaatt gttacgtatt atataagtta ttatagaatt attctattag 4560
106 aatatacgat gaaaaaagta tgtatatatta attgtcacta attttatgtt tattgattta 4620
107 tacttttgaa ggaagagcat cttgagatcg cgagggccaa gaaggaacta ggagagtcag 4680
108 aattaaattg ggatgattac aagaaaatgg actttactca atgtgtatgt tactatcatt 4740
109 ctcatatttt attctatgtt catatgattt atgatgaaac caaaattatt gatttttttt 4800
110 ttggtgtgtg tgaaggttat aaatgaaact cttcgattgg gaaatgtagt taggtttttg 4860
111 catcgcaaag cactcaaaga tgttcggtac aaaggtaaaa ctttacgtac aaaattttta 4920
112 aataatgaaa tccggaatat tgaaatctta ttggatgaaa aatattaaaa taatttacat 4980
113 ttcttaatgt tggaaaaaag gatacgatat ccctagtggg tggaaagtgt taccggtgat 5040
114 ctgagccgta catttgata attctcgta tgaccaacct aatctcttta atccttgag 5100
115 atggcaacag gtaataaaaa agtttctctc gttaactatc gaaaattagt gtatagtttt 5160
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117 agaactatta atctggcaaa aactttttat tattattatc tttcaagtta gatcttaaca 5280
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122 atgacttgta cgtgcgttag attctgccac gttgactggg ttttaacttt agatttataa 5580
123 ctctattaat tataacaact atcaaatcgg cgaattagag aaatatacta tatagtatta 5640
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126 ccaacaagca cgtgttcttc ttcttttttt cttcccaact tctttttttg ggggtttatt 5820
127 gtgatttata aaatcggttt gtcgtttttt tttgtgacga gcagcaaaac aacggagcgt 5880
128 catcgtcagg aagtggtagt ttttcgacgt ggggaaacaa ctacatgccg tttggaggag 5940
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131 ttgttgattt tcctaacggt ttgcctatta ggggttctcg tattctgtaa aaaaaaaaaa 6120
132 agatgaaagt atttttattc tcttcttttt tttttgataa ttttaaatca ttttttttgc 6180
133 ccaatgatat ataaaaattt ggataaataa tattattgga tattcgtttt ttagttcggg 6240
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135 gagtcttttg acatttgtat tggatgttgt tgattattag tgtcgacact attaaacctt 6360
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138 actcgtgtgt gtctagtggg aaatcattgg gctggagact gaacatcaga acacaagaaa 6540
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146 &lt;210&gt; SEQ ID NO: 2

147 &lt;211&gt; LENGTH: 513

148 &lt;212&gt; TYPE: PRT

149 &lt;213&gt; ORGANISM: Arabidopsis thaliana

151 &lt;400&gt; SEQUENCE: 2

152 Met Phe Glu Thr Glu His His Thr Leu Leu Pro Leu Leu Leu Pro

153 1 5 10 15

154 Ser Leu Leu Ser Leu Leu Leu Phe Leu Ile Leu Leu Lys Arg Arg Asn

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155          20          25          30
156 Arg Lys Thr Arg Phe Asn Leu Pro Pro Gly Lys Ser Gly Trp Pro Phe
157          35          40          45
158 Leu Gly Glu Thr Ile Gly Tyr Leu Lys Pro Tyr Thr Ala Thr Thr Leu
159          50          55          60
160 Gly Asp Phe Met Gln Gln His Val Ser Lys Tyr Gly Lys Ile Tyr Arg
161 65          70          75          80
162 Ser Asn Leu Phe Gly Glu Pro Thr Ile Val Ser Ala Asp Ala Gly Leu
163          85          90          95
164 Asn Arg Phe Ile Leu Gln Asn Glu Gly Arg Leu Phe Glu Cys Ser Tyr
165          100          105          110
166 Pro Arg Ser Ile Gly Gly Ile Leu Gly Lys Trp Ser Met Leu Val Leu
167          115          120          125
168 Val Gly Asp Met His Arg Asp Met Arg Ser Ile Ser Leu Asn Phe Leu
169          130          135          140
170 Ser His Ala Arg Leu Arg Thr Ile Leu Leu Lys Asp Val Glu Arg His
171 145          150          155          160
172 Thr Leu Phe Val Leu Asp Ser Trp Gln Gln Asn Ser Ile Phe Ser Ala
173          165          170          175
174 Gln Asp Glu Ala Lys Lys Phe Thr Phe Asn Leu Met Ala Lys His Ile
175          180          185          190
176 Met Ser Met Asp Pro Gly Glu Glu Glu Thr Glu Gln Leu Lys Lys Glu
177          195          200          205
178 Tyr Val Thr Phe Met Lys Gly Val Val Ser Ala Pro Leu Asn Leu Pro
179          210          215          220
180 Gly Thr Ala Tyr His Lys Ala Leu Gln Ser Arg Ala Thr Ile Leu Lys
181 225          230          235          240
182 Phe Ile Glu Arg Lys Met Glu Glu Arg Lys Leu Asp Ile Lys Glu Glu
183          245          250          255
184 Asp Gln Glu Glu Glu Glu Val Lys Thr Glu Asp Glu Ala Glu Met Ser
185          260          265          270
186 Lys Ser Asp His Val Arg Lys Gln Arg Thr Asp Asp Asp Leu Leu Gly
187          275          280          285
188 Trp Val Leu Lys His Ser Asn Leu Ser Thr Glu Gln Ile Leu Asp Leu
189          290          295          300
190 Ile Leu Ser Leu Leu Phe Ala Gly His Glu Thr Ser Ser Val Ala Ile
191 305          310          315          320
192 Ala Leu Ala Ile Phe Phe Leu Gln Ala Cys Pro Lys Ala Val Glu Glu
193          325          330          335
194 Leu Arg Glu Glu His Leu Glu Ile Ala Arg Ala Lys Lys Glu Leu Gly
195          340          345          350
196 Glu Ser Glu Leu Asn Trp Asp Asp Tyr Lys Lys Met Asp Phe Thr Gln
197          355          360          365
198 Cys Val Ile Asn Glu Thr Leu Arg Leu Gly Asn Val Val Arg Phe Leu
199          370          375          380
200 His Arg Lys Ala Leu Lys Asp Val Arg Tyr Lys Gly Tyr Asp Ile Pro
201 385          390          395          400
202 Ser Gly Trp Lys Val Leu Pro Val Ile Ser Ala Val His Leu Asp Asn
203          405          410          415

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204 Ser Arg Tyr Asp Gln Pro Asn Leu Phe Asn Pro Trp Arg Trp Gln Gln  
 205 420 425 430  
 206 Gln Asn Asn Gly Ala Ser Ser Ser Gly Ser Gly Ser Phe Ser Thr Trp  
 207 435 440 445  
 208 Gly Asn Asn Tyr Met Pro Phe Gly Gly Gly Pro Arg Leu Cys Ala Gly  
 209 450 455 460  
 210 Ser Glu Leu Ala Lys Leu Glu Met Ala Val Phe Ile His His Leu Val  
 211 465 470 475 480  
 212 Leu Lys Phe Asn Trp Glu Leu Ala Glu Asp Asp Gln Pro Phe Ala Phe  
 213 485 490 495  
 214 Pro Phe Val Asp Phe Pro Asn Gly Leu Pro Ile Arg Val Ser Arg Ile  
 215 500 505 510

216 Leu

219 &lt;210&gt; SEQ ID NO: 3

220 &lt;211&gt; LENGTH: 24

221 &lt;212&gt; TYPE: DNA

222 &lt;213&gt; ORGANISM: Artificial Sequence

224 &lt;220&gt; FEATURE:

225 &lt;223&gt; OTHER INFORMATION: Primer: D4OVERF

227 &lt;400&gt; SEQUENCE: 3

228 atgttcgaaa cagagcatca tact

24

230 &lt;210&gt; SEQ ID NO: 4

231 &lt;211&gt; LENGTH: 21

232 &lt;212&gt; TYPE: DNA

233 &lt;213&gt; ORGANISM: Artificial Sequence

235 &lt;220&gt; FEATURE:

236 &lt;223&gt; OTHER INFORMATION: Primer: D4PRM

238 &lt;400&gt; SEQUENCE: 4

239 cctcgatcaa agagagagag a

21

241 &lt;210&gt; SEQ ID NO: 5

242 &lt;211&gt; LENGTH: 29

243 &lt;212&gt; TYPE: DNA

244 &lt;213&gt; ORGANISM: Artificial Sequence

246 &lt;220&gt; FEATURE:

247 &lt;223&gt; OTHER INFORMATION: Primer: D4RTF

249 &lt;400&gt; SEQUENCE: 5

250 ttcttggtga aaccatcggt tatcttaaa

29

252 &lt;210&gt; SEQ ID NO: 6

253 &lt;211&gt; LENGTH: 26

254 &lt;212&gt; TYPE: DNA

255 &lt;213&gt; ORGANISM: Artificial Sequence

257 &lt;220&gt; FEATURE:

258 &lt;223&gt; OTHER INFORMATION: Primer: D4RTR

260 &lt;400&gt; SEQUENCE: 6

261 tatgataagc agttcctggt agattt

26

263 &lt;210&gt; SEQ ID NO: 7

264 &lt;211&gt; LENGTH: 21

265 &lt;212&gt; TYPE: DNA

266 &lt;213&gt; ORGANISM: Artificial Sequence

**RAW SEQUENCE LISTING ERROR SUMMARY**  
**PATENT APPLICATION: US/09/502,426B**

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Input Set : A:\11696-070001.txt  
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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:25; Xaa Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22  
Seq#:25; Xaa Pos. 23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,42,43,46  
Seq#:25; Xaa Pos. 48,50,56,57,58,61,62,63,64,65,66,67,68,72,82,92,93,94,95  
Seq#:25; Xaa Pos. 96,97,102,107,108,111,112,113,114,126,128,136,138,142,146  
Seq#:25; Xaa Pos. 148,149,153,154,156,160,163,165,166,168,175,178,180,183  
Seq#:25; Xaa Pos. 184,185,186,190,193,197,201,203,204,206,207,208,209,212  
Seq#:25; Xaa Pos. 213,216,217,218,219,221,228,229,230,232,233,236,237,239  
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Seq#:25; Xaa Pos. 284,287,288,289,290,291,292,293,294,295,296,298,300,302  
Seq#:25; Xaa Pos. 306,307,308,309,310,311,312,313,314,315,316,317,318,319  
Seq#:25; Xaa Pos. 320,321,322,323,324,325,326,334,336,337,338,339,340,341  
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Seq#:26; Xaa Pos. 4,8,10  
Seq#:28; Xaa Pos. 1,13,15,16